

Outline of Microarray Chip Technology approach

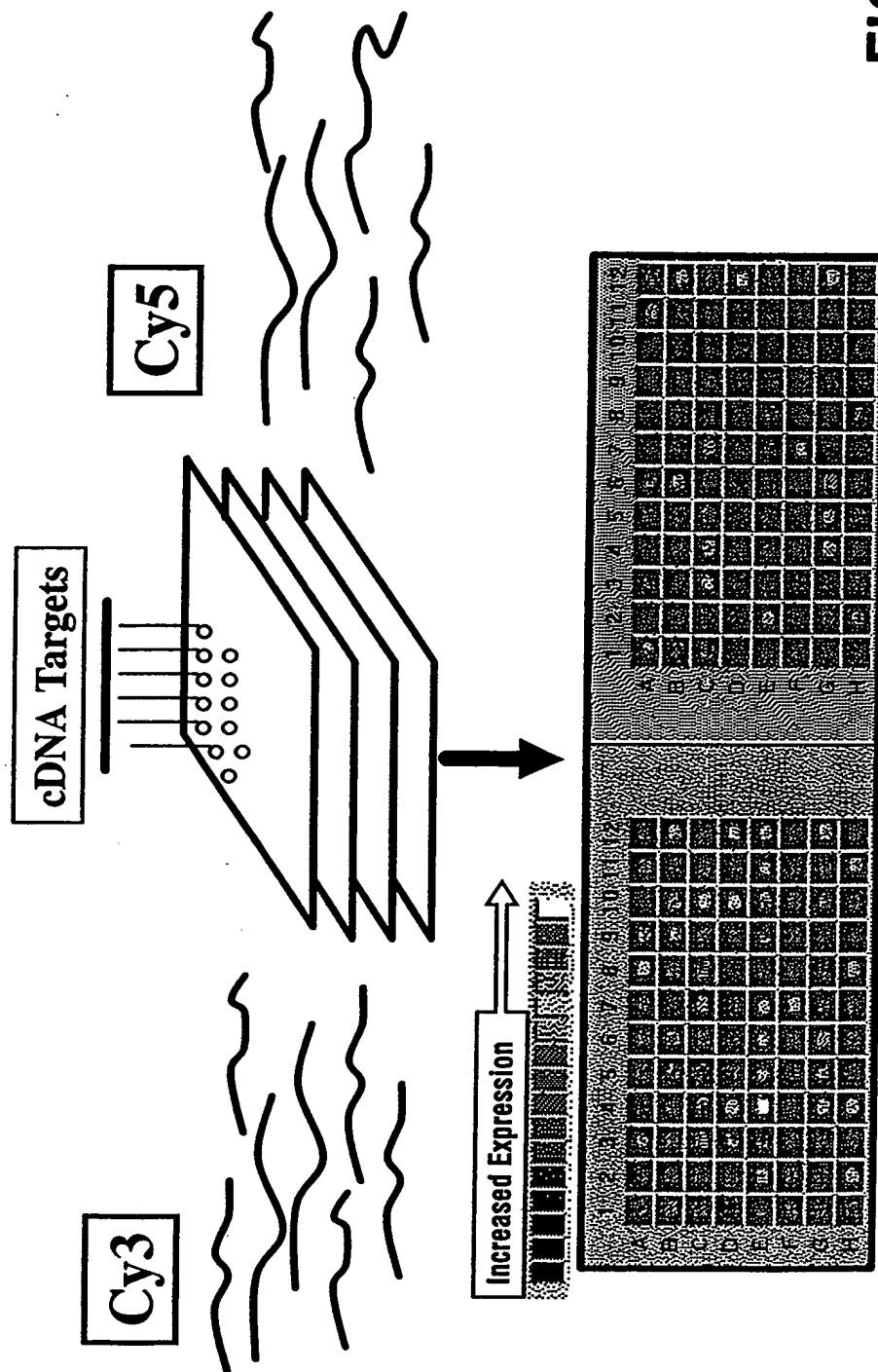


FIG. 1

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General protocol for *in-vitro* whole gene CD8 T cell priming

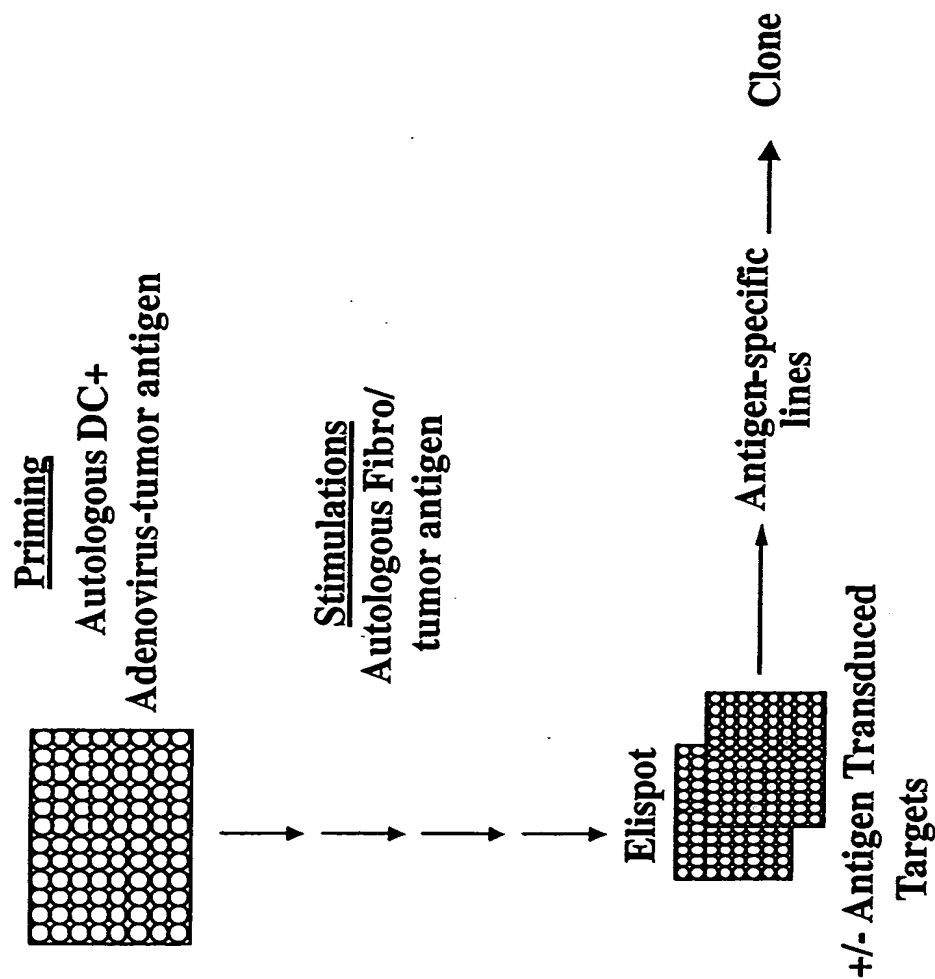


FIG. 2

General protocol for *in-vitro* whole gene CD4 T cell priming

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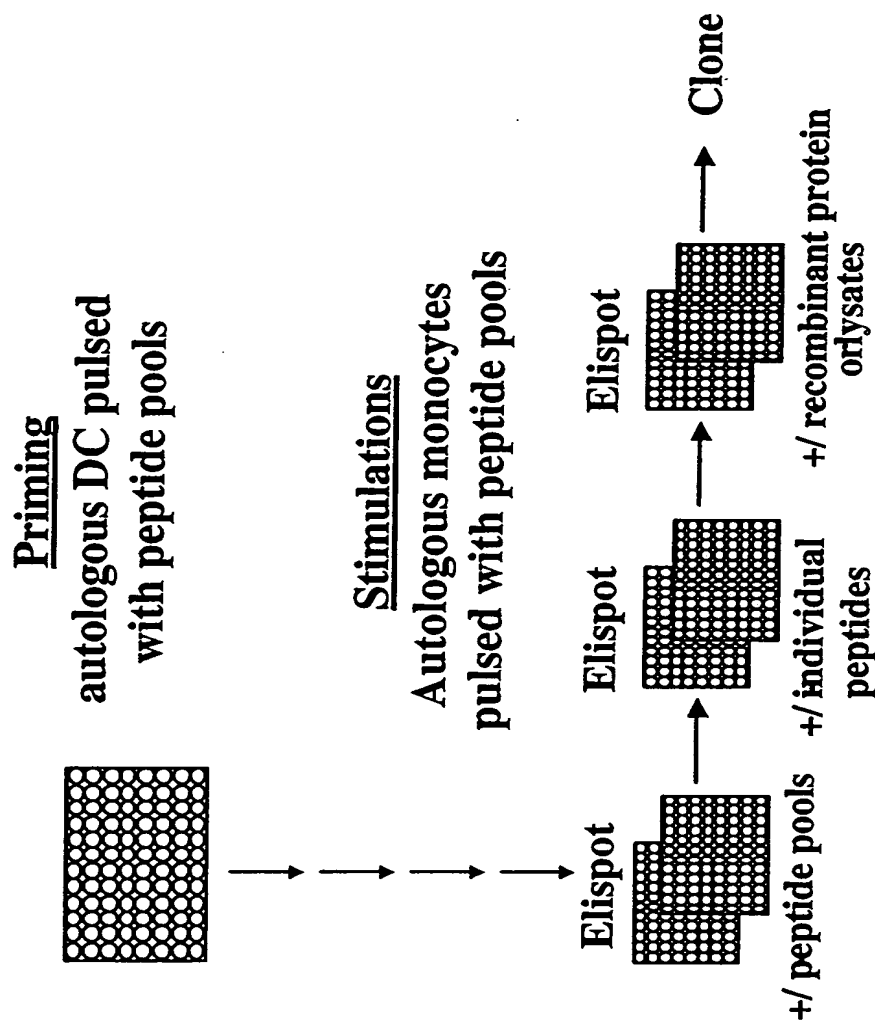


FIG. 3

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LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.**RED:** Normal essential tissue probes where gene expression is to be avoided.**BLACK:** Normal tissue probes where gene expression is acceptable.**FIG. 4**

Hematology Therapeutic Ab Candidates

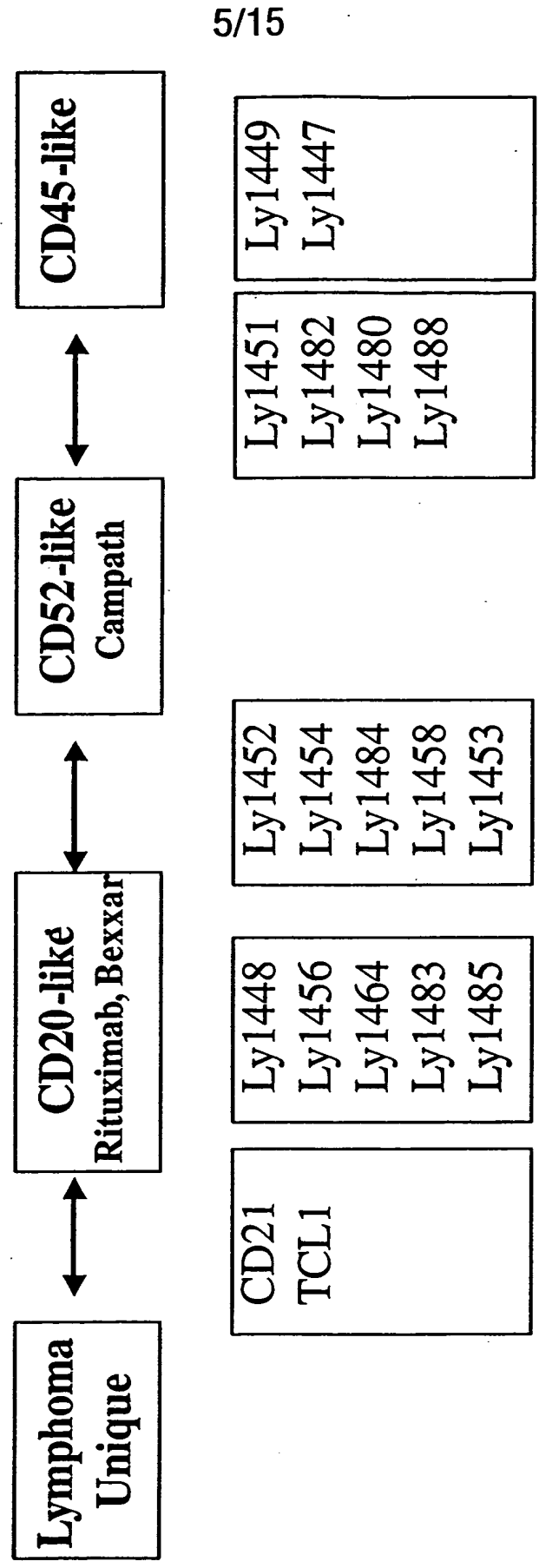


FIG. 5

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a. TMpred Report for Ly1484 Long

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
 TQKLVEKLYSGMFSADPRHLLFILEHIMVVE TASSORDIVLSTLYSSL
 NKVILYCLSKPQOOSLSECLGLLSILGLFLOEHWDVVFAT YNSNISFLLCLM
 HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
 QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
 ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
 DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
 EQLFGEGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
 HKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES
 LHSEDFLELCRERQVILQELLDKKVTQKFSLVIVQGHVSEGVLLFGHQ
 HFYICENFTLSPTECDVYCHRHCLSNISDPFIFNLCSKDRSTDHYSCQCHS
 YADMRELROARFLLQDIALEIFFHNGYSKFLV FYNNDRSKAFKSFCSFQP
 SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTC
 NDYMQYPVPFVWLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR
 FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTQAFCALQ GCSFD
 VADRMFHSVKSTWESASRENMSDVRELTPPEFFYLPEFLNCGNEVEFGCMQ
 DCTVLCDVQLPPWADEDPRKFTSLHRKALESDFVSANLHHWIDLIFCYKQ
 QCPAAVDVAVNIFHPYFYCDRMDLSSITDPLIKSTILGFVSNFCQVPKQLF
 TKPHPARTAACKPLPKKDVSTPVSLLPCHPQPFYSLQSLRPSQVIVKDMY
 LFSLGESESPKCACTHIVSTEKTLAVERNKVLLPPLWNRTFSWGFDDFSC
 CLCSYCSKVLMEFENLAAWGRCLCAVCPSPTTIVTSETSTVVCVWELSM
 TKERPRGLRLRQALYZHTQAVTCLAASVTFSLVSGESQDCTCTLLNDLHL
 THVTRLPAHREGISAITISDVSETIVSCAGHLSLWNVNGOPLASTTAW
 GPEGAITCCCLMECPAWDTSQIITITESQDGMVRVWKTEEDVKMSVPCRPAG
 EEPLAQPPSPRGHKWEKNLALSRELDVSTALTEKPSKTS PAVTALA VSRN
 HFKLLVCDERERTFCWSADG (SEQ ID NO: 120)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,
 Blue = EXTRACELLULAR

Ly1484 Long has 1269 amino acids and 5
 Transmembrane Domains

Transmembrane Domain 1: 63 - 84	Score: 1.36675
Transmembrane Domain 2: 118 - 139	Score: 1.38695
Transmembrane Domain 3: 480 - 501	Score: 1.36185
Transmembrane Domain 4: 562 - 583	Score: 1.31785
Transmembrane Domain 5: 725 - 746	Score: 1.3521

FIG. 6

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b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
 ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
 AIIVASYLVRMPFFTQAFCAIQCGSFDVADRMFHSVKSTWESASRENMSD
 VRELTPPEFFYLPEFLTNCNGVEFCGMODGTVLEDVOLPPWADGDPKFTIS
 LHRKALESDFVSANLHHWIDLTFCYKQOCPAAVDAVNIFHPYFYCDRMDL
 SSITDPLIKSTILCFVSNFCQVPKQLFTKPHIPARTAAACKPLPKGDVSTPV
 SLPGHPQPFYSLQSLRPSQVTVKDMVLFSLGSESPKCAIGHIVSTKKT
 LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYCSDKVLMITFENLAAWERC
 LCAVCPSPPTTIVTSGTSTVVCVWELSMTEKCRPRCLRLROALYCHTQAVTC
 LAASVTFSLVSGSQDCTCTLLNDLDHILTHVTRLPAHREGTSAITISDVSC
 TIVSCACAHLSLWNVNGOPLASTTFAWCPEGATTCCLMECPAWDTSQIT
 ITGSDQGMVRVWKTEEDVKMSVPCRPAGEEPLAOPPSPRCHKWEKNLALSR
 ELDVSTALTCKPSKTSPTAVTALAVSRNHFKLLVGEDERGRIFCWSADG

(SEQ ID NO: 121)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,
 Blue = EXTRACELLULAR

Ly1484 has 646 amino acids and 1 Transmembrane
 Domains

Transmembrane Domain 1: 102 - 123 Score: 1.3521

FIG. 6 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file--> LY1484-1.TXT
 Beginning with residue: 1 and ending with residue: 1270
 AMPHI Window size: 11

A-AMPHI mid points of blocks.
 R-Residues matching the Rothbard/Taylor motif.
 D-Residues matching the IAd motif.
 d-Residues matching the IEd motif.

(SEQ ID NO: 120)

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	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAPSLANISCFQKLVEKLYSGMFSADPRHILLFIL															
.....AAAAA.....AAAA.AAA.....AAAA.AAAAAA.....															
.....RRRRR..RRRRRR.....RRRRRRRRRR.....RRRRRRRRRR.....															
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....															
.....RRRRR..RRRRRR.....RRRRRRRRRR.....RRRRRRRRRR.....															
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....															
.....RRRRR..RRRRRR.....RRRRRRRRRR.....RRRRRRRRRR.....															
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....															
.....RRRRR..RRRRRR.....RRRRRRRRRR.....RRRRRRRRRR.....															
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....															

FIG. 7

[illegible]

FIG. 7 (cont.)

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455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDEKVKTKFSLVIVQGHLVSEGVLFFGHQHFYICENFTLSPTGVDYCTRHCLSN
...AAAAA...RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..AAAA
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPFIFNLCKDRSTDHYSCQCHSYADMRELROARFLLQDIALEIFFHNHGYSKFLVFYNNDRSKAFKSFCSFQP
A.AAAAAA.....AAAAAA....RRRRRRRRRRRR.....RRRR.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSETLNLRYPGSDRIMLKWKQRDISNFEYLMYLNTAAGRTCNDYMQVPFPWVLADYTSETLNLAN
.....AAAAA.....AAA.....AAAAAAAAA.....RRRRRRRR.....RRRRRRRR.....
DDDDDD.....
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIFRDLSKPMGAQTKERKLKFIORFKEVEKTEGDMTVQCHYYTHYSSAIIVASLYVRMPPTQAFCALQGSFD
AAAAAAAAAAAAA.....AAAAAA.....RRRR.RRRRR.....RRRR.....R

```

FIG. 7 (cont.)

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.....DDDDDDDDDD.....
.....ddd.....
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKRFISLH
AAAAAAAAAAAA.AA.AAAA.AAAAAA.....AAA.....
RRRRRRR.....RRRRR.....RRRRR.....RRRR..
.....
.....
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900
RKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
.....AAAAAAAA.....AAAAAAAAAAAAAA
.RRRR.RRRR.....RRRR.....RRRR.....
.....DDDDDD.....
.....
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975
TKPHPARTAAGKPLPGKDVSTPVSPLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTILA
.....AAAAAAA.....AAAAAA
.....RRRR
.....DDDDDD.....DDDDDD
.....

FIG. 7 (cont.)

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```

980 985 990 995 1000 1000 1010 1015 1020 1025 1030 1030 1040 1045 1050
VERNKVLLPPLWNRFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAVCPSTTIVTSGTSTVVCWELSM
.....AAAAA.....
.....RRRR.....
.....DDDDDDDDDD.....
.....
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
TKGRPRGLRLRQALYGHTQAVTCLAAASVTFSLVSGSDCTCILWDLDHLTHVTRLPAHREGISAITISDVSGTI
.....AAAAA.....
.....RRRRRR.....
DDD...DDDDDD.....DDDDDD.....DDDDDD
.dddddd.....
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
VSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
A.....AAA.....AAAAAA.....
RR.....RRRR.....RRRRRR.....
D.....DDDDDD.....DDDDDD.....
.....
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....
.....RRRR.....
.....DDDDDDDD.....DDDDDDDD.....
.....

```

FIG. 7 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

FIG. 8

[illegible]

These are the results of the analysis of the file--> LY1484~2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A-AMPHI mid points of blocks.
R-Residues matching the Rothbard/Taylor motif.
D-Residues matching the IAd motif.
d-Residues matching the IEd motif.

(SEQ ID NO: 121)

[illegible]

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
 QRFKEVETEGDMTVQCHYVTHYSSAIIVASYLVRMPPTQAFCALQGSFDVADRMFHSVKSTWESASRENMSD
 AAAAAAAAAA.....AAAAA.....AAAAAAAAAAAA.AA.AAAA.AA.
 R.....RRRRR.RRRRR.....RRRRRRR.....
DDDDDDDDDD.....

```

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKFI SLHRKALESDFVSANLHHWIDLIFGY
AAAA.....AAAAAA
..RRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....

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230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGPAAVDVNIHFHYPFYGDRLSSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAAGKPLPGKDVSTPV
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKILAVERNKVLLPPLWNRTFSWGFDDE
AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR
D...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSDKVLMTFENLAAWGRCLCAVCPSTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAVTC
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLVSGSQDCTCILWDLDLHDLTHVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITT
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR
DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD
...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD

```

FIG. 8 (cont.)

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530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
.....AAAAAAA
RRRR.....
D.....DDDDDD
.....

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRR.....
DDDDDDDD.....ddddd
.....

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FIG. 8 (cont.)

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